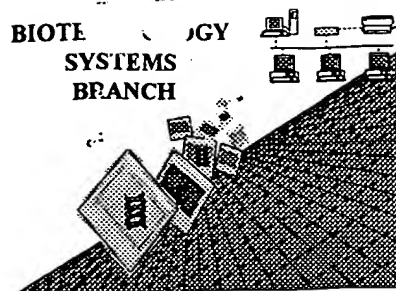


RAW SEQUENCE LISTING **ERROR REPORT**



6-5-01
RECEIVED
MAY 30 2001
TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/728,421A
Source: 1632
Date Processed by STIC: 5/16/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1632

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/728,421A

DATE: 05/16/2001
 TIME: 09:54:40

Input Set : A:\A-579D.txt
 Output Set: N:\CRF3\05162001\I728421A.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Yoshinaga, Steven
 5 <120> TITLE OF INVENTION: Novel Polypeptides Involved in Immune Response
 7 <130> FILE REFERENCE: A-579D
 9 <140> CURRENT APPLICATION NUMBER: 09/728,421A
 10 <141> CURRENT FILING DATE: 2000-11-28
 12 <160> NUMBER OF SEQ ID NOS: 35
 14 <170> SOFTWARE: PatentIn version 3.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 600
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Mouse
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (1)..(600)
 25 <400> SEQUENCE: 1

26	atg aag ccg tac ttc tgc cgt gtc ttt gtc ttc tgc ttc cta atc aga	48
27	Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg	
28	1 5 10 15	
30	ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca	96
31	Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser	
32	20 25 30	
34	ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc	144
35	Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val	
36	35 40 45	
38	cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa	192
39	Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu	
40	50 55 60	
42	ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca	240
43	Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro	
44	65 70 75 80	
46	atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta	288
47	Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu	
48	85 90 95	
50	aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc	336
51	Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser	
52	100 105 110	
54	att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat	384
55	Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr	
56	115 120 125	
58	ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta	432
59	Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu	
60	130 135 140	
62	ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata	480
63	Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile	
64	145 150 155 160	
66	ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac	528
67	Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp	

0.4

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/728,421A
 DATE: 05/16/2001
 TIME: 09:54:40

Input Set : A:\A-579D.txt
 Output Set: N:\CRF3\05162001\I728421A.raw

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68          165          170          175
70 cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag      576
71 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
72          180          185          190
74 tct aga ctt gca ggt gtg acc tca      600
75 Ser Arg Leu Ala Gly Val Thr Ser
76          195          200
79 <210> SEQ ID NO: 2
80 <211> LENGTH: 200
81 <212> TYPE: PRT
82 <213> ORGANISM: Mouse
84 <400> SEQUENCE: 2
86 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
87 1          5          10          15
90 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
91          20          25          30
94 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
95          35          40          45
98 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
99          50          55          60
102 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
103 65          70          75          80
106 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
107          85          90          95
110 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
111          100          105          110
114 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
115          115          120          125
118 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
119          130          135          140
122 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
123 145          150          155          160
126 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
127          165          170          175
130 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
131          180          185          190
134 Ser Arg Leu Ala Gly Val Thr Ser
135          195          200
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 200
140 <212> TYPE: PRT
141 <213> ORGANISM: Mouse
143 <400> SEQUENCE: 3
145 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
146 1          5          10          15
148 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
149          20          25          30
151 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
152          35          40          45

```

RAW SEQUENCE LISTING

DATE: 05/16/2001

PATENT APPLICATION: US/09/728,421A

TIME: 09:54:40

Input Set : A:\A-579D.txt

Output Set: N:\CRF3\05162001\I728421A.raw

```

154 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
155      50      55      60
157 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
158 65      70      75      80
160 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
161      85      90      95
163 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
164      100      105      110
166 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
167      115      120      125
169 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
170      130      135      140
172 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
173 145      150      155      160
175 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
176      165      170      175
178 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
179      180      185      190
181 Ser Arg Leu Ala Gly Val Thr Ser
182      195      200
184 <210> SEQ ID NO: 4
185 <211> LENGTH: 218
186 <212> TYPE: PRT
187 <213> ORGANISM: Mouse
189 <400> SEQUENCE: 4
191 Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Asn Phe Phe Ser Val Gln
192 1      5      10      15
194 Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val
195      20      25      30
197 Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
198      35      40      45
200 Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
201      50      55      60
203 Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
204 65      70      75      80
206 Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
207      85      90      95
209 Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
210      100      105      110
212 Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
213      115      120      125
215 Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
216      130      135      140
218 Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
219 145      150      155      160
221 Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
222      165      170      175
224 Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met
225      180      185      190

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/728,421A

DATE: 05/16/2001
TIME: 09:54:40

Input Set : A:\A-579D.txt
Output Set: N:\CRF3\05162001\I728421A.raw

227 Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
228 195 200 205
230 Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
231 210 215
233 <210> SEQ ID NO: 5
234 <211> LENGTH: 234
235 <212> TYPE: PRT
C--> 236 <213> ORGANISM: Artificial
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Synthetic
241 <220> FEATURE:
242 <221> NAME/KEY: misc feature
243 <223> OTHER INFORMATION: Unspecified amino acid
246 <400> SEQUENCE: 5
W--> 248 Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg
249 1 5 10 15
W--> 251 Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
252 20 25 30
W--> 254 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
255 35 40 45
W--> 257 Val Xaa Xaa Ser Cys Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
258 50 55 60
W--> 260 Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Cys Xaa
261 65 70 75 80
W--> 263 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
264 85 90 95
W--> 266 Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Val Xaa Phe Xaa Leu
267 100 105 110
W--> 269 Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Phe Cys Xaa Xaa Xaa
270 115 120 125
W--> 272 Xaa Xaa Xaa Pro Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Gly Xaa
273 130 135 140
W--> 275 Xaa Xaa His Ile Xaa Glu Xaa Xaa Leu Cys Xaa Xaa Xaa Xaa Xaa
276 145 150 155 160
W--> 278 Lys Leu Xaa Trp Xaa Leu Xaa Val Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa
279 165 170 175
W--> 281 Xaa Xaa Leu Leu Xaa Xaa Xaa Xaa Leu Xaa Xaa Ile Trp Xaa Xaa Xaa
282 180 185 190
W--> 284 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa
285 195 200 205
W--> 287 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg
288 210 215 220
W--> 290 Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
291 225 230
293 <210> SEQ ID NO: 6
294 <211> LENGTH: 966
295 <212> TYPE: DNA
296 <213> ORGANISM: Mouse
298 <220> FEATURE:

see item 11 on Error Summary sheet

This error
appears in
subsequent
sequences, too.

response: Xaa is
an
unspecified
amino acid.

Per 1.823 of
Sequence Rules,
<222> and response
are mandatory
whenever Xaa's (or
n's) are present in
the sequence

Please Note:

Use of n and/ r Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

PSI:

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/728,421A

DATE: 05/16/2001

TIME: 09:54:41

Input Set : A:\A-579D.txt

Output Set: N:\CRF3\05162001\I728421A.raw

L:236 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:248 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:251 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:254 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:257 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:260 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:263 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:266 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:269 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:272 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:275 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:278 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:281 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:284 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:287 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:290 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:619 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:631 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:634 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:637 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:640 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:643 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:646 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:649 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:652 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10

VERIFICATION SUMMARY

DATE: 05/16/2001

PATENT APPLICATION: US/09/728,421A

TIME: 09:54:41

Input Set : A:\A-579D.txt

Output Set: N:\CRF3\05162001\I728421A.raw

L:655 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:658 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:661 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:664 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:667 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:670 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:670 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:673 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:673 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:676 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:679 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:682 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:685 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:688 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:691 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:978 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:990 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:990 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:993 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:996 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:996 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:999 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:999 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1002 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1005 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1005 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1008 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1011 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1014 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1017 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1020 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1020 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15

VERIFICATION SUMMARY

DATE: 05/16/2001

PATENT APPLICATION: US/09/728,421A

TIME: 09:54:41

Input Set : A:\A-579D.txt

Output Set: N:\CRF3\05162001\I728421A.raw

L:1023 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
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L:1026 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1026 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1029 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1029 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1371 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:1695 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:1707 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:1719 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:1731 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:1743 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:1755 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:1767 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:1779 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:1791 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:1803 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:1815 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35

RAW SEQUENCE LISTING

DATE: 05/16/2001

PATENT APPLICATION: US/09/728,421A

TIME: 09:54:40

Input Set : A:\A-579D.txt

Output Set: N:\CRF3\05162001\I728421A.raw

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299 <221> NAME/KEY: CDS
300 <222> LOCATION: (1)..(966)
302 <400> SEQUENCE: 6
303 atg cag cta aag tgt ccc tgt ttt gtg tcc ttg gga acc agg cag cct      48
304 Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro
305 1                    5                    10                    15
307 gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt      96
308 Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
309                    20                    25                    30
311 ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act      144
312 Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
313                    35                    40                    45
315 gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac      192
316 Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
317 50                    55                    60
319 ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa      240
320 Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
321 65                    70                    75                    80
323 atc gaa aac cca gaa gtt tcg gtg act tac tac ctg cct tac aag tct      288
324 Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
325                    85                    90                    95
327 cca ggg atc aat gtg gac agt tcc tac aag aac agg ggc cat ctg tcc      336
328 Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
329 100                    105                    110
331 ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc      384
332 Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
333 115                    120                    125
335 acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca      432
336 Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
337 130                    135                    140
339 gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg      480
340 Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
341 145                    150                    155                    160
343 gca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac      528
344 Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
345 165                    170                    175
347 ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca      576
348 Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
349 180                    185                    190
351 gag ccc aac ctg tat tgg atc aac aca acg gac aat agc cta ata gac      624
352 Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
353 195                    200                    205
355 acg gct ctg cag aat aac act gtc tac ttg aac aag ttg ggc ctg tat      672
356 Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
357 210                    215                    220
359 gat gta atc agc aca tta agg ctc cct tgg aca tct cgt ggg gat gtt      720
360 Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
361 225                    230                    235                    240
363 ctg tgc tgc gta gag aat gtg gct ctc cac cag aac atc act agc att      768

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